



UNC
GILLINGS SCHOOL OF
GLOBAL PUBLIC HEALTH

BIOSTATISTICS SEMINAR



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The University of Pennsylvania

Heterogeneity: from bulk tissue to single cells

Heterogeneity in various features (e.g., genotype, gene expression and phenotype) prevails not only between individuals within a population but also between cells within each individual, and even between cells of the same cell type from the same individual. In this talk, I will present statistical methods to study heterogeneity from two different perspectives. First, I will present a Bayesian framework for cancer clonal history inference. I will show that, by repeated bulk sequencing of temporally and/or spatially separated tumor specimens from the same patient, one can identify the underlying mixture components of the tumor and recover its clonal history. In the second part of the talk, I will present how to use single-cell RNA sequencing to better understand cellular heterogeneity. I will discuss how to model transcriptional bursting at the allelic level, while accounting for the technical noise in single-cell RNA sequencing.

Thursday, January 26, 2017

3:30 pm - 4:30 pm

Blue Cross Blue Shield Auditorium

0001 Michael Hooker Research Center